In the Claims:

1. (**Currently Amended**) A method of using statistical analysis of genetic data from an inbred population to determine likely genetic regions for a recessive genetic disease or trait, comprising the steps of:

obtaining actual genotype data from members of an inbred population, wherein said members are selected from one or both of: people affected with a genetic disease or trait in said inbred population and parents of people affected with said genetic disease or trait in said inbred population;

obtaining estimated genotype data for said inbred population; and

analyzing the actual and estimated genotype data to find a region in genomes of the affected people **or a region in genomes of parents of the affected people,** ~~that~~ **wherein said region** includes markers exhibiting particular homozygous pairs of alleles more frequently than would occur randomly~~, wherein~~ **and** said step of analyzing is performed using a computing device, and wherein said step of analyzing comprises:

determining a set of scores under various assumptions for each of said markers in said actual and estimated genotype data relative to each person for which actual genotype data was determined, with the ~~assumptions for each marker including at least that the marker is autozygous and that the marker is not autozygous~~ **set of scores for each marker including at least first scores generated to determine probabilities of observing each marker given autozygosity with the founder and second scores generated to determine probabilities of observing each marker given absence of autozygosity with the founder**;

merging the set of scores for each marker to **produce a** ~~arrive at a first~~ merged score for each marker, **wherein said step of merging comprises** ~~the first merged score being determined under an assumption that the marker is autozygous, and a second merged score for each marker, the second merged score being determined under an assumption that the marker is not autozygous;~~

~~———~~computing for each of said markers a ratio of **said first scores to said second scores** ~~said first merged score to said second merged score to produce marker scores~~,

wherein each ~~of said marker~~ **merged** scores indicates at least in part a statistical

distinction between whether said marker is autozygous and whether said marker is not autozygous;

examining ~~said marker~~ **the merged** scores to determine one or more contiguous regions of markers ~~with a high sum of marker scores~~ **by locating a statistically significant gap in sums of said merged scores for non-overlapping contiguous regions of markers, wherein contiguous regions of markers having scores above the gap are determined to be said one or more contiguous regions of markers**;

selecting from said one or more contiguous regions of markers at least one contiguous region likely to contain a recessive allele associated with said genetic disease or trait; and

~~reporting~~ **storing** said at least one contiguous region likely to contain a recessive allele associated with said genetic disease or trait to a **computer-readable memory** ~~user of said computing device~~.

2. (Previously Presented) A method as in claim 1, wherein said inbred population is a relatively inbred population with a higher occurrence of said genetic disease or trait than a more general population.

3. (Previously Presented) A method as in claim 2, wherein the particular homozygous pairs of alleles are autozygous alleles descended from a founder of said genetic disease or trait in said relatively inbred population.

4. (**Currently Amended**) A method as in claim 3, wherein **each** ~~said marker~~ **merged** score for a marker represents a comparison of a likelihood of observing said marker given that people with said genetic disease or trait are autozygous at said marker versus a likelihood of observing said marker given that alleles for said marker are independent of said genetic disease or trait.

5. (**Currently Amended**) A method as in claim 4, wherein said marker receives a higher ~~marker~~ **merged** score from one form of homozygosity versus another form of

homozygosity, with the form receiving said higher score being more likely to be associated with said genetic disease or trait.

6. (**Currently Amended**) A method as in claim 5, wherein said ~~marker~~ **merged** scores are placed in an array ordered by a chromosomal order of markers associated with the scores.

7. (**Currently Amended**) A method as in claim 6, wherein identifying said at least one ~~particular~~ **contiguous** region further comprises determining a consecutive portion of said array that has the highest sum.

8. (**Currently Amended**) A method as in claim 6, wherein identifying said at least one ~~particular~~ **contiguous** region further comprises computing all sums of a predetermined fixed number of adjacent elements in said array and comparing the sums.

9. (Cancelled)

10. (**Canceled**)

11. (**Currently Amended**) A method of analyzing actual and estimated genotype data, with the actual genotype data obtained for one or more affected people with the genetic disease or trait in an inbred population, for their parents, or for the affected people and their parents, and with the estimated genotype data obtained for said population, the method performed to find a region in genomes of the affected people **or a region in genomes of parents of the affected people,** ~~that~~ **wherein said region** includes markers exhibiting particular homozygous pairs of alleles more frequently than would occur randomly, the method comprising:

determining a set of scores under various assumptions for each marker in said actual and estimated genotype data relative to each person for which actual genotype

data was determined, with the ~~assumptions for each marker including at least that the marker is autozygous and that the marker is not autozygous~~ **set of scores for each marker including at least first scores generated to determine probabilities of observing each marker given autozygosity with the founder and second scores generated to determine probabilities of observing each marker given absence of autozygosity with the founder**;

merging the set of scores for each marker to **produce a** ~~arrive at a first~~ merged score for each marker, **wherein said step of merging comprises** ~~the first merged score being determined under an assumption that the marker is autozygous, and a second merged score for each marker, the second merged score being determined under an assumption that the marker is not autozygous;~~

~~———~~computing for each of said markers a ratio of **said first scores to said second scores** ~~said first merged score to said second merged score to produce marker scores~~,

wherein each ~~of said marker~~ **merged** scores indicates at least in part a statistical distinction between whether said marker is autozygous and whether said marker is not autozygous;

examining ~~said marker~~ **the merged** scores to determine one or more contiguous regions of markers ~~with a high sum of marker scores~~ **by locating a statistically significant gap in sums of merged scores for non-overlapping contiguous regions of markers, wherein contiguous regions of markers having scores above the gap are determined to be said one or more contiguous regions of markers**;

selecting from said one or more contiguous regions of markers at least one contiguous region likely to contain a recessive allele associated with said genetic disease or trait; and

~~reporting~~ **storing** said at least one contiguous region likely to contain a recessive allele associated with said genetic disease or trait to a **computer-readable memory** ~~user of said computing device~~;

wherein said determining and merging steps are performed using a computing device.

12. (Previously Presented) A method as in claim 11, wherein said population is a relatively inbred population with a higher occurrence of said genetic disease or trait than a more general population.

13. (Previously Presented) A method as in claim 12, wherein the particular homozygous pairs of alleles are autozygous alleles descended from a founder of said genetic disease or trait in said relatively inbred population.

14. (**Currently Amended**) A method as in claim 13, wherein **each** ~~said marker~~ **merged** score for a marker represents a comparison of a likelihood of observing said marker given that people with said genetic disease or trait are autozygous at said marker versus a likelihood of observing said marker given that alleles for the marker are independent of said genetic disease or trait.

15. (**Currently Amended**) A method as in claim 14, wherein said marker receives a higher ~~marker~~ **merged** score from one form of homozygosity versus another form of homozygosity, with the form receiving said higher score being more likely to be associated with said genetic disease or trait.

16. (**Currently Amended**) A method as in claim 15, wherein said ~~marker~~ **merged** scores are placed in an array ordered by a chromosomal order of markers associated with the scores.

17. (**Currently Amended**) A method as in claim 16, wherein identifying said at least one ~~particular~~ **contiguous** region further comprises determining a consecutive portion of said array that has the highest sum.

18. (**Currently Amended**) A method as in claim 16, wherein identifying said at least one ~~particular~~ **contiguous** region further comprises computing all sums of a predetermined fixed number of adjacent elements in said array and comparing the

sums.

19. (Cancelled)

20. (**Canceled**)

21. (**Currently Amended**) An apparatus including:

a processor;

input and output interfaces; and

a memory storing instructions executable by the processor to analyze actual and estimated genotype data, with the actual genotype data obtained for one or more affected people with the genetic disease or trait in an inbred population, for their parents, or for the affected people and their parents, and with the estimated genotype data obtained for said population, the method performed to find a region in genomes of the affected people **or a region in genomes of parents of the affected people,** ~~that~~ **wherein said region** includes markers exhibiting particular homozygous pairs of alleles more frequently than would occur randomly, the instructions including steps of: (a) determining a set of scores under various assumptions for each marker in said actual and estimated genotype data relative to each person for which actual genotype data was determined, with the ~~assumptions for each marker including at least that the marker is autozygous and that the marker is not autozygous~~ **set of scores for each marker including at least first scores generated to determine probabilities of observing each marker given autozygosity with the founder and second scores generated to determine probabilities of observing each marker given absence of autozygosity with the founder**; (b) merging the set of scores for each marker to **produce a** ~~arrive at a first~~ merged score for each marker, **wherein said step of merging comprises** ~~the first merged score being determined under an assumption that the marker is autozygous, and a second merged score for each marker, the second merged score being determined under an assumption that the marker is not autozygous; (c)~~ computing for each of said markers a ratio of **said first scores to said second scores**

~~said first merged score to said second merged score to produce marker scores~~, wherein each ~~of said marker~~ **merged** scores indicates at least in part a statistical distinction between whether said marker is autozygous and whether said marker is not autozygous; ~~(d)~~ **(c)** examining ~~said marker~~ **the merged** scores to determine one or more contiguous regions of markers ~~with a high sum of marker scores~~ **by locating a statistically significant gap in sums of merged scores for non-overlapping contiguous regions of markers, wherein contiguous regions of markers having scores above the gap are determined to be said one or more contiguous regions of markers**; ~~(e)~~ **(d)** selecting from said one or more contiguous regions of markers at least one contiguous region likely to contain a recessive allele associated with said genetic disease or trait; and (f) ~~reporting~~ **storing** said at least one contiguous region likely to contain a recessive allele associated with said genetic disease or trait to a **computer-readable memory** ~~user of said computing device~~.

22. (Previously Presented) A method as in claim 1, further comprising the step of sequencing said at least one contiguous region likely to contain a recessive allele associated with said genetic disease or trait.

23. (Previously Presented) A method as in claim 11, further comprising the step of sequencing said at least one contiguous region likely to contain a recessive allele associated with said genetic disease or trait.